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RAW SEQUENCE LISTING

DATE: 04/21/2003

PATENT APPLICATION: US/09/905,743B

TIME: 13:14:11

Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF4\04212003\I905743B.raw

3 <110> APPLICANT: Chadwick, Brian Paul
4 Frischauf, Anna Maria
6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES
AND NUCLEIC

7 ACIDS
9 <130> FILE REFERENCE: 28110/36120C
11 <140> CURRENT APPLICATION NUMBER: 09/905,743B
12 <141> CURRENT FILING DATE: 2001-07-13
14 <150> PRIOR APPLICATION NUMBER: 09/240,639
15 <151> PRIOR FILING DATE: 1999-01-29
17 <160> NUMBER OF SEQ ID NOS: 32
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2762
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo Sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (232)..(1599)
29 <223> OTHER INFORMATION:

W--> 32 <400> 1

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37 gcgcggtgca tggaatgggc tatgtgaatg aaaaaaggta tccgttatga aacttcaga      180
39 aaaacgagct acatttttca gcagccgcag caggttcctt ggcaacaag g atg aga      237
40                                     Met Arg
41                                     1
43 aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc      285
44 Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
45      5      10      15
47 ctg ggg ctg tgt gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg      333
48 Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
49      20      25      30
51 cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc      381
52 His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
53 35      40      45      50
55 ccg ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct      429
56 Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
57      55      60      65
59 gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc      477
60 Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
61      70      75      80
63 act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa      525
64 Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu

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65	85	90	95	
67	act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt	573		
68	Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu			
69	100 105 110			
71	tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa	621		
72	Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu			
73	115 120 125 130			
75	cta ctg gat gtt gct aaa cag gac att ccg ttc gac ttc tgg aag gcc	669		
76	Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala			
77	135 140 145			
79	acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga	717		
80	Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly			
81	150 155 160			
83	gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca	765		
84	Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala			
85	165 170 175			
87	tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca	813		
88	Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr			
89	180 185 190			
91	gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc	861		
92	Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser			
93	195 200 205 210			
95	ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga	909		
96	Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly			
97	215 220 225			
99	gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag	957		
100	Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln			
101	230 235 240			
103	gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc	1005		
104	Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr			
105	245 250 255			
107	tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca	1053		
108	Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala			
109	260 265 270			
111	cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga	1101		
112	Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly			
113	275 280 285 290			
115	aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg	1149		
116	Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp			
117	295 300 305			
119	gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca	1197		
120	Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala			
121	310 315 320			
123	agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac	1245		
124	Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn			
125	325 330 335			
127	aga gtg cac agg acg gag gaa gtg aag cat gtg gac ttc tat gct ttc	1293		
128	Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe			
129	340 345 350			

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131 tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag      1341
132 Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
133 355                      360                      365                      370
135 aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac      1389
136 Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr
137                      375                      380                      385
139 gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc      1437
140 Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
141                      390                      395                      400
143 atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc      1485
144 Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
145                      405                      410                      415
147 agg agc aaa gtg ctg aag ctc act cgg aaa att gac aat gtt gag acc      1533
148 Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
149                      420                      425                      430
151 agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga      1581
152 Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
153 435                      440                      445                      450
155 cag aag agt cca gcc tca tagtgggcga gccatccctg tccccgtcag      1629
156 Gln Lys Ser Pro Ala Ser
157                      455
159 cagtgtctgt gtgtctgcat aaacctcct gtccctggacg tgacttcac ctagaggagcc      1689
161 acagcacagg ccgtgctggc actttctgca cactggctct gggacttgca gaaggcctgg      1749
163 tgctgccctg gcacagcct cttccagtc catctggcca gagggtctgc tggacctggg      1809
165 ccctgtctaa tgccacctgt ctgcctgggc tccaagtggg caggaccagg acagaaccac      1869
167 aggcacacac tgagggggca gtgtggctcc ctgcctgtcc catccccatg ccccgctccg      1929
169 ggggtctgtg ctgctgctgt gcatgtccct gcgatgggag tcttgtctcc cagcctgtca      1989
171 gtttctctcc cagggcagag ctcctcttcc tgcaagagtc tgggaggcgg tgcaggctgt      2049
173 cctggctgct ctggggaagc cgagggacag ccataacacc cccgggacag taggtctggg      2109
175 cggcaccact gggaactctg gacttgagtg tgtttgtct tcttgggta tgaatgtgtg      2169
177 agttcaccca gaggcctgct ctctcacac attgtgtggt ttgggggttaa tgatggaggg      2229
179 agacacctct tcatagacgg caggtgccc cctttcaggg agtctcccag catgggcgga      2289
181 tgccgggcat gagctgctgt aaactatttg tggtgtgtgt gcttgagtga cgtctctgtc      2349
183 gtgtgggtgc caagtgttg ttagaaaact gtgttctgag ccccttttc tggacaccaa      2409
185 ctgtgtcctg tgaatgtatc gctactgtga gctgttcccg cctagccagg gccatgtctt      2469
187 aggtgcagct gtgccacggg tcagctgagc cacagtccca gaaccaagct ctcggtgtct      2529
189 cgggccacca tccgcccacc tcgggtgac cccacctcct ccatggacag tgtgagcccc      2589
191 gggccgtgca tctgtctcag tgtggcgtca gtgtcggggc tgagccctt gagctgcttc      2649
193 agtgaatgta cagtgcctgg cactgagctga acctcatgtg ttccactccc aataaaaggt      2709
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199 <211> LENGTH: 456
200 <212> TYPE: PRT
201 <213> ORGANISM: Homo Sapiens
203 <400> SEQUENCE: 2
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206 1                      5                      10                      15
209 Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
210                      20                      25                      30

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213 Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
214      35      40      45
217 Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
218      50      55      60
221 Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
222 65      70      75      80
225 Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
226      85      90      95
229 Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
230      100     105     110
233 Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
234      115     120     125
237 Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
238      130     135     140
241 Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
242 145     150     155     160
245 Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
246      165     170     175
249 Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
250      180     185     190
253 Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
254      195     200     205
257 Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
258      210     215     220
261 Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
262 225     230     235     240
265 Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
266      245     250     255
269 Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
270      260     265     270
273 Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
274      275     280     285
277 Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
278      290     295     300
281 Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
282 305     310     315     320
285 Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
286      325     330     335
289 Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
290      340     345     350
293 Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
294      355     360     365
297 Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
298      370     375     380
301 Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
302 385     390     395     400
305 Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
306      405     410     415
309 Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val

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Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF4\04212003\I905743B.raw

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310          420          425          430
313 Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu
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317 Asn Arg Gln Lys Ser Pro Ala Ser
318          450          455
321 <210> SEQ ID NO: 3
322 <211> LENGTH: 2797
323 <212> TYPE: DNA
324 <213> ORGANISM: Homo Sapiens
326 <220> FEATURE:
327 <221> NAME/KEY: CDS
328 <222> LOCATION: (83)..(1669)
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336          Met Phe Thr Val Leu Thr Arg Gln Pro Cys
337          1          5          10
339 gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc      160
340 Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
341          15          20          25
343 ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc      208
344 Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
345          30          35          40
347 atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt      256
348 Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
349          45          50          55
351 att gtg ctg gat gcc ggg tct tca aga acc aca gtc tac gtg tat caa      304
352 Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
353          60          65          70
355 tgg cca gca gaa aaa gag aat aat acc gga gtg gtc agt caa acc ttc      352
356 Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
357 75          80          85          90
359 aaa tgt agt gtg aaa ggc tct gga atc tcc agc tat gga aat aac ccc      400
360 Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
361          95          100          105
363 caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg      448
364 Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
365          110          115          120
367 cag gtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc      496
368 Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
369          125          130          135
371 acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat      544
372 Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
373          140          145          150
375 gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac      592
376 Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
377 155          160          165          170
379 ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga      640

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VERIFICATION SUMMARY

DATE: 04/21/2003

PATENT APPLICATION: US/09/905,743B

TIME: 13:14:12

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L:332 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:329
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L:924 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:921